

Tue Jun 26 17:54:16 2001

4x633148.res

perfect matches in Ig V domain
Seq No: 18, 12, 13, 8, 5

Page 1

> O <
O I O Intelligence
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 4x633148.res made by spaula on Tue 26 Jun 101 17:53:40-PDT.

Query sequence being compared: US-08-633-148-4 (1-318)
Number of sequences searched: 18
Number of scores above cutoff: 14

Results of the initial comparison of US-08-633-148-4 (1-318) with:
File: us08_633148_mod.pep

100-

N

U

M

B

E

R

Q

F

S

E

Q

U

E

N

C

E

S

SCORE

STDEV

1

35

71

141

106

177

212

247

283

318

4

*

PARAMETERS

Similarity matrix Unitary K-tuple 2
Mismatch penalty 5 Joining penalty 20
Gap penalty 1.00 Window size 318
Gap size penalty 0.26
Cutoff score 0
Randomization group 0

SEARCH STATISTICS

Scores: Mean Median 11 Standard Deviation 72.45

Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 507
Number of sequences searched: 18
Number of scores above cutoff: 18

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

Sequence Name Description Length Score Score Init. Opt.

1. US-08-633-148-4 Sequence 4, Application US 318 318 4.02 0

The list of other best scores is:

Sequence Name	Description	Length	Score	Init. Opt.	Sig. Frame
2. US-08-633-148-18	Sequence 18, Application	16	16	16	-0.15 0
3. US-08-633-148-12	Sequence 12, Application	15	15	15	-0.17 0
4. US-08-633-148-15	Sequence 15, Application	11	11	11	-0.22 0
5. US-08-633-148-9	Sequence 9, Application US	11	11	11	-0.22 0
6. US-08-633-148-10	Sequence 10, Application	14	14	14	-0.22 0
7. US-08-633-148-17	Sequence 17, Application	10	10	10	-0.23 0
8. US-08-633-148-16	Sequence 16, Application	10	10	10	-0.23 0
9. US-08-633-148-13	Sequence 13, Application	10	10	10	-0.23 0
10. US-08-633-148-11	Sequence 11, Application	10	10	10	-0.23 0
11. US-08-633-148-8	Sequence 8, Application US	10	10	10	-0.23 0
12. US-08-633-148-7	Sequence 7, Application US	10	10	10	-0.23 0
13. US-08-633-148-5	Sequence 5, Application US	11	11	11	-0.23 0
14. US-08-633-148-21	Sequence 21, Application	11	11	11	-0.23 0
15. US-08-633-148-20	Sequence 20, Application	11	11	11	-0.23 0
16. US-08-633-148-6	Sequence 6, Application	11	11	11	-0.23 0
17. US-08-633-148-14	Sequence 14, Application	9	9	9	-0.25 0
18. US-08-633-148-19	Sequence 19, Application	10	9	9	-0.25 0

1. US-08-633-148-4 (1-318)

US-08-633-148-4 Sequence 4, Application US/08633148

Initial Score = 318 Optimized Score = 318 Significance = 4.02
Residue Identity = 100% Matches = 318 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

X 10 20 30 40 50 60 70
AONTARIGEPVLKCKGAPKPPORLEKLTGTETAWKVLSPQGGGWDVSVARVLPNGSLFPAVGIODE
|||||
AONTARIGEPVLKCKGAPKPPORLEKLTGTETAWKVLSPQGGGWDVSVARVLPNGSLFPAVGIODE
X 10 20 30 40 50 60 70

GIFRCAMNRNGKETKSNRYRVYQIPGKPEIVDSASELTAGVFNKVCSEGYPAAGTILSHWLDGKPLVP
|||||
GIFRCAMNRNGKETKSNRYRVYQIPGKPEIVDSASELTAGVFNKVCSEGYPAAGTILSHWLDGKPLVP
|||||

150 160 170 180 190 200 210
NEKGVSVKEQTRRHPTGLTLOSELAVTPARGDPRPTSCFSGLPRHRLATAPIQVRVPEVPLEEY
|||||
NEKGVSVKEQTRRHPTGLTLOSELAVTPARGDPRPTSCFSGLPRHRLATAPIQVRVPEVPLEEY
150 160 170 180 190 200 210

220 230 240 250 260 270 280
OLVVEPEGAVAGGTVTLTCEVPAQPSQIHWKMDGVPLPLPSPVLILPEIGPDQGTSCVATHSSHGP
|||||
OLVVEPEGAVAGGTVTLTCEVPAQPSQIHWKMDGVPLPLPSPVLILPEIGPDQGTSCVATHSSHGP
220 230 240 250 260 270 280

290 300 310 X
QESRAVSISIIIEPEGPTAGSVGGGLGT
|||||
QESRAVSISIIIEPEGPTAGSVGGGLGT
290 300 310 X

2. US-08-633-148-4 (1-318)

US-08-633-148-4 Sequence 18, Application US/08633148

Initial Score = 16 Optimized Score = 16 Significance = -0.15
Residue Identity = 100% Matches = 16 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

X 10 20 30 40 50 60
AONTARIGEPVLKCKGAPKPPORLEKLTGTETAWKVLSPQGGGWDVSVARVLPNGSLFPA

|||||
AQNITARIGEPVLVK
X 10 X

3. US-08-633-148-4 (1-318)

US-08-633-148-12 Sequence 12, Application US/08633148

Initial Score = 15 Optimized Score = -0.17
Residue Identity = 100% Matches = 15 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

X 10 X 20 30 40 50 60
AQNITARIGEPVLVKCKGAPKPPQRLKMKLNTGRTEAMKVLSPQGGPWSVARVLPNGSLFLP
|||||
AQNITARIGEPVLVK
X 10 X

4. US-08-633-148-4 (1-318)

US-08-633-148-15 Sequence 15, Application US/08633148

Initial Score = 11 Optimized Score = -0.22
Residue Identity = 100% Matches = 11 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

130 140 150 160 170 180 X 190
GSYPAGTSLSHLDGKPLVPNEKGVSKQTRRHPTGLTLOSELMTVPARGDPRPTFSFSPGLPRHRA
|||||
RGDDPRPTFS
X 10

200 210 220 230
LRTAPIQPRWEPVPLEEVQLVVEGGAVAGGTTLT

5. US-08-633-148-4 (1-318)

US-08-633-148-9 Sequence 9, Application US/08633148

Initial Score = 11 Optimized Score = -0.22
Residue Identity = 100% Matches = 11 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

190 200 210 220 230 240 X
SFSPLPRHRLTAPIQPRWEPVPLEEVQLVVEGGAVAGGTTLTCEVPAQSPQIHWKMDGVPLPL
|||||
CEVPAQSPQI
X 10

260 270 280 290
PPSPVLILPEIGPDQGTYSVATHSHGQPQESRAVSIS

6. US-08-633-148-4 (1-318)

US-08-633-148-10 Sequence 10, Application US/08633148

Initial Score = 11 Optimized Score = -0.22
Residue Identity = 85% Matches = 12 Mismatches = 2
Gaps = 0 Conservative Substitutions = 0

30 40 50 60 70 X 80 90
LEWKLNTGRTEAMKVLSPQGGPWSVARVLPNGSLFLPAVGIDEGIFRCQAMNRNGKETKSNRYRVYQI
|||||
CRAMNQNGKETKSN
X 10 X

100 110 120 130 140
PGKPEIVDSASELTAGVPKNVGTCTVSEGSYPAGTSLSHLDGK

7. US-08-633-148-4 (1-318)

US-08-633-148-17 Sequence 17, Application US/08633148

Initial Score = 10 Optimized Score = -0.23
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

240 250 260 270 280 X 290 X 300
TLTCEVPAQSPQIHWKMDGVPLPLPPSVLILPEIGPDQGTYSVATHSHGQPQESRAVSISIIIEPGEEG
|||||
SSHGPOESRA
X 10

310
PTAGSVGGSGGLGT

8. US-08-633-148-4 (1-318)

US-08-633-148-16 Sequence 16, Application US/08633148

Initial Score = 10 Optimized Score = -0.23
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

140 150 160 170 180 190 X 210
GKPLVPNEKGVSKQTRRHPTGLTLOSELMTVPARGDPRPTFSFSPGLPRHRLTAPIQPRWEP
|||||
SPGLPRHRL
X 10

220 230 240
VPLEEVQLVVEGGAVAGGTTLTCEVPAQSPQIH

9. US-08-633-148-4 (1-318)

US-08-633-148-13 Sequence 13, Application US/08633148

Initial Score = 10 Optimized Score = -0.23
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

10 X 20 X 30 40 50 60 70
AQNITARIGEPVLVKCKGAPKPPQRLKMKLNTGRTEAMKVLSPQGGPWSVARVLPNGSLFLPAVGIDQE
|||||
CKGAPKPPQ
X 10

GIF

10. US-08-633-148-4 (1-318)

US-08-633-148-11 Sequence 11, Application US/08633148

Initial Score = 10 Optimized Score = -0.23
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

220 230 240 250 260 270 X 290
VEEGAVAGGTTLTCEVPAQSPQIHWKMDGVPLPLPPSVLILPEIGPDQGTYSVATHSHGQPQES
|||||
GPDDQGTYS
X 10

300 310
RAVSISIIIEPGEEGTAGSVGGSGGLGT

11. US-08-633-148-4 (1-318)

US-08-633-148-8 Sequence 8, Application US/08633148

Initial Score = 10 Optimized Score = -0.23
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

10 20 30 X 50 60 70

US-08-633-148-4 (1-318)
26 17:54:16 2001

AQNITARIGEPLVLCKGAPKPPORLEWKLNTGRTAWKVLSPQGGPMDSVARVLPNGSLFLPAVGIOQE
|||||
WKLNTGRTA
X 10

80
GIFRCQAMNRNGKETK

12. US-08-633-148-4 (1-318)
US-08-633-148-7 Sequence 7, Application US/08633148

Initial Score = 10 Optimized Score = 10 Significance = -0.23
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0
220 230 240 250 260 270 X 290
VEPEGAVAPGGTVLTCEVPAQSPQIHWKDKGVLPPLPSPVLILPEIGPDQGTYSVATHSHGQDES
|||||
GPDQGTYS
X 10

300
RAVSISIIPEGEGTAGSVGGSLGT

13. US-08-633-148-4 (1-318)
US-08-633-148-5 Sequence 5, Application US/08633148

Initial Score = 10 Optimized Score = 10 Significance = -0.23
Residue Identity = 100% Matches = 10 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0
10 X 20 X 30 X 40 X 50 X 60 X 70
AQNITARIGEPLVLCKGAPKPPORLEWKLNTGRTAWKVLSPQGGPMDSVARVLPNGSLFLPAVGIOQE
|||||
CKGAPKPPQ
X 10

GIF

14. US-08-633-148-4 (1-318)
US-08-633-148-21 Sequence 21, Application US/08633148

Initial Score = 10 Optimized Score = 10 Significance = -0.23
Residue Identity = 90% Matches = 10 Mismatches = 1
Gaps = 0 Conservative Substitutions = 0
240 250 260 270 280 X 290 X 300
TLTCEVPAQSPQIHWKDKGVLPPLPSPVLILPEIGPDQGTYSVATHSHGQESRAVSISIERGEEG
|||||
SSHGQESRAC
X 10

310
PRAGSVGGSLGT

15. US-08-633-148-4 (1-318)
US-08-633-148-20 Sequence 20, Application US/08633148

Initial Score = 10 Optimized Score = 10 Significance = -0.23
Residue Identity = 90% Matches = 10 Mismatches = 1
Gaps = 0 Conservative Substitutions = 0
140 150 160 170 180 190 X
DGKPLVPNEKGVSKQTRRRHPETGLFTLOSELMTVPARGGDPRTFSCFSPGLPRHRLRTAPIQPVWE
|||||
CSPGLPRHRL
X 10

210 220 230 240
PVPLEEVQLVVEPEGAVAPGGTVTLTCEVPAQSPQIHW

16. US-08-633-148-4 (1-318)
US-08-633-148-6 Sequence 6, Application US/08633148

Initial Score = 10 Optimized Score = 10 Significance = -0.23
Residue Identity = 90% Matches = 10 Mismatches = 1
Gaps = 0 Conservative Substitutions = 0
10 20 30 X 50 60 70
AQNITARIGEPLVLCKGAPKPPORLEWKLNTGRTAWKVLSPQGGPMDSVARVLPNGSLFLPAVGIOQE
|||||
WKLNTGRTA
X 10

80
GIFRCQAMNRNGKETK

17. US-08-633-148-4 (1-318)
US-08-633-148-14 Sequence 14, Application US/08633148

Initial Score = 9 Optimized Score = 9 Significance = -0.25
Residue Identity = 100% Matches = 9 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0
110 120 130 140 150 X 160 170
EIVDSASELTAGVPNKVGTVCVSEGSYPAGTLSWHLDGKPLVPNEKGVSKQTRRRHPETGLFTLOSELMTVP
|||||
EQTRRHPE
X X

180 190 200 210
ARGGDPRTFSCFSPGLPRHRLRTAPIQPVWE

18. US-08-633-148-4 (1-318)
US-08-633-148-19 Sequence 19, Application US/08633148

Initial Score = 9 Optimized Score = 9 Significance = -0.25
Residue Identity = 90% Matches = 9 Mismatches = 1
Gaps = 0 Conservative Substitutions = 0
110 120 130 140 150 X 170
PEIVDSASELTAGVPNKVGTVCVSEGSYPAGTLSWHLDGKPLVPNEKGVSKQTRRRHPETGLFTLOSELMTVP
|||||
EQTRRHPE
X X

180 190 200 210
PARGGDPRTFSCFSPGLPRHRLRTAPIQPVWE